



SNOR motif

| | | |
|---------|-----|---|
| SMRTER: | 573 | KEEILLMQIQKVDNETKSAETTMTETLRKKKESIMEEAALAKEQRAAKELND |
| mN-CoR: | 177 | KEELIQSMDRVDREIAKVEQQILKLKKKQQQLEEEA--AKPPEPEKPVSP |
| hSMRT: | 169 | KEELIQNMDRVDREITMVEQQISKLKKKQQQLEEEA--AKPPEPEKPVSP |
| SMRTER: | 623 | NNNDQEPMVVELSWRSQMLAEKTYAANKRTAQRCHSMLQNAAADESSPGSV |
| mN-CoR: | 226 | -----PPVEQKHRS--IVQIIYDENRKKAEAEAHKIFEGGLGPKVE---- |
| hSMRT: | 217 | -----PPIESKHRS--LVQIIYDENRKKAEAAHRILEGLGPOVE---- |
| SMRTER: | 673 | AGRPWLPLYNQHLVDEALAMLTROHQSQIRAPLLHLIRKLKAERWAHNOG |
| mN-CoR: | 263 | -----LPLYNQPSDTKVYHENIKINQV-MRKKLILFFKRRNHARKQREQK |
| hSMRT: | 254 | -----LPLYNQPSDTROYHENIKINQA-MRKKLILYFKRRNHARKQWKQK |
| SMRTER: | 723 | LVEKYTKDQADWQRRCEERMEASAKRKAREAKNREFFFEKVFIELRKQREDK |
| mN-CoR: | 307 | ICQRYDQLMEAWKKVDRIENNP RRKAKESKTREY YEKQFP EIRKQREQQ |
| hSMRT: | 298 | FCQRYDQLMEALEKKVERIENNP RRKAKESKVREY YEKQFP EIRKQRELQ |
| SMRTER: | 773 | ERFN-RVGSR-----IKSEADLEIMDGLQEQALEDKKMRSYAVIPP |
| mN-CoR: | 357 | ERFQ-RVGQRGAGLSATTHARSEHEISEIIDGLSEQENNEKQMRQLSVIPP |
| hSMRT: | 348 | ERMOSRVGQRGSGLSMSAARSEHEVSEIIDGLSEQENLEKQMRQLAVIPP |
| SMRTER: | 814 | LMHDARQRRRCAYHNENGLIEDMVAVHQQRKALNM |
| mN-CoR: | 406 | MMFDAEQRRVKFINMNGLMEDPMKVYKDROFMNV |
| hSMRT: | 398 | MLYDADQORIKFINMNGLMADPMKVYKDROVMNM |

SANT domain

| | | | |
|------------|------|--|--------|
| SMRTER | :848 | WTAGEKETFKKEYLQHPKNFGATAASLDR-KSPQDCVRYYYLSKKTENY | 100% |
| mN-CoR(1): | 440 | WTDHEKEIFKDKFIQHPKNFGGLIASYLER-KSVDPDCVLYYYLTCKKNENY | 68/80% |
| hSMRT(1): | 432 | WSEQEKETFREKFMQHPKNFGGLIASFLER-KTVABCVLYYYLTCKKNENY | 64/82% |
| C14B9.6 | :615 | WSPEERSLFLKSROADHVKIFHGLTEFFVD-KTASDILVLFYYMNNKKTEDY | 35/53% |
| CF53H10 | :218 | WTPDEIYQFQDAIYQSEKDFDKVAVELPG-KSVKECVQFYFYTWKDCPD | 38/56% |
| xER1 | :277 | WTEEECRNFEQGLKAIGKDFHLIQANKVRTRSVGECVAFYYMWKKSERV | 36/56% |
| mN-CoR(2): | 627 | WTEEEEMEVAKKGLVEHGRNWAATAK-MVGTKSEADCKNFYFNKRRHNL | 34/53% |
| hSMRT(2): | 615 | WTEEEEMETAKKGLLEHGRNWSAIAAR-MVGSHTVSQCKNFYFNKRRQNL | 38/57% |
| hKIAA0071: | 106 | WTVKDKVLFEEQAFSFKIFHRIQQMLPD-KSIASLVKFYYSWKKTRTK | 37/50% |
| CMTA-I | :198 | WTDQEITLTFENCYQIFGKNFSQIRSEALCH-RSLOSIVQFYYESKKRVKY | 39/51% |
| YCR592 | :673 | FIDDEHSLELEGYLIHPKKFGKISHYMGGLRSPEECVTHYVRTKKTIVNY | 46/62% |

α-helix

α-helix

ITS motif

| | | |
|---------|------|------------------|
| SMRTER: | 2424 | TRQIVMHDYITSQQMO |
| SMRT: | 1681 | NRQTIINDYITSQQMH |
| N-CoR: | 1615 | TRQTIINDYITSQQMO |

GSI motif

| | | |
|----------|------|-----------------|
| SMRTER: | 2274 | VKSGSIIHGTPANS |
| | 2236 | GKHGSITQGTPLHM |
| SMRT: | 1203 | VPGGSITKGTIPSTR |
| | 1224 | TYRGSITHGTPADV |
| | 1350 | HIRGSITQGTIPRSY |
| | 1446 | LKEGSITQGTPLKY |
| | 1517 | SSGGSITARGAPVIV |
| N-CoR: | 921 | TPPGSILISSPIKP |
| | 1064 | IMGGSISQGTTPGT |
| | 1092 | PSVGSISLGLPRQQ |
| | 1149 | VQEGSITRGTPASK |
| | 1171 | SLRGSITQGTPLP |
| | 1302 | VLSGSIMQGTPRAT |
| | 1388 | IEGSISQGTPIKF |
| C14B9.6: | 920 | QTQGSLSGTTPFQA |

LSD motif

| | | |
|---------|------|--------------------|
| SMRTER: | 3430 | ESKPLLLSKYDALSD-ED |
| SMRT: | 2501 | EPKPLLCQYETLSDS |
| N-CoR: | 2436 | EPAPLLSAQYETLSDD |

FIGURE 9